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                                                                                         322.6
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Gapop 10.0 , Gapext 1.0
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10426.099 Million cell updates/sec
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gb_gss2:*
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814
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635
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                                   CN148454
CN126847
CK208301
                                                                                         BM140351
CF487085
                                                                                                                  CB659172
AU162766
CD225047
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CB656525
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AI906433
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                                                                                                                                                                                    CB683938
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AI906433 IL-BT109-
CD307119 StrPu691.
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CCC1 37 H
WHE0474 D
POL1 41 D
WOUND1 15
WOUND1 56
RHOH1 19
FGAS02000
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1 StrPu691.
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RESULT 1 BI376242

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CF488266	CF487230	CF432900	CD224549	CF485910	CD222873	CN133040	CD227467	CD229216	CF481017	CD223689	BG241153	CG440030	CN127041	BE041110	BE040798	CD429468	CA269770	CB902534	CB903555	CA227320
CF488266 POL1_48_F) POL1_42	_19	CD224549 CCC1_34_E	0 POL1 34	CCCI 24		CD227467 CCC1_51_G	6 CCC1_:	CF481017 POL1_69_B	CD223689 CCC1_29_A	≅	CG440030 OGVHP10TH	CN127041 RHOH1_20_	BE041110 OF19H01 O	BE040798 OF11G11 O	CD429468 ETH1_4_D0	CA269770 SCMCRT308	CB902534 tric030xk	CB903555 tric035xc	CA227320 SCJLFL301

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM COMMENT DEFINITION FOCUS JÖURNAL MEDLINE TITLE PUBMED Email: panopoul@molgen.mpg.de The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones giving the same hybridisation pattern with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well the coordinates of the rest of the clones assigned to the same fingerprint cluster as the clone from which the above BST is generated is available at the amphioxus project site at: http://www.molgen.mpg.de/amphioxus/ Clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de) Insert Length: 1200 Std Error: 0.00 Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86 FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3 laboratory 145, dept.Lehrach Max-Planck-Institut fuer Molekulare Genetik Ihnestr.63-73, D-14195 Berlin, Germany Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J Herwig, R., Vingron, M. and Lehrach, H. New evidence for genome-wide duplications at the origin of mRNA sequence. BI376242 BI376242.1 GI:30911206 BI376242 623 bp mRNA linear EST 26-AUG-200: BFLG3_000038 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNA clone MPMGp498A1518 5', Branchiostoma floridae (Florida lancelet) Branchiostoma floridae PCR PRimers Tel: +49 30 8413 1235 Fax: +49 30 8413 1128 vertebrates using an amphioxus Contact: Panopoulou G Eukaryota; Metazoa; 2683279 Genome Res. 13 (6A), 1056-1066 (2003) Branchiostoma (bases 1 to 623) Chordata; Cephalochordata; Branchiostomidae; gene set and completed animal 3' (M13FSP) Poustka, A.J., EST 26-AUG-2003

Euteleostomi;

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RESULT 2
A1906433/c
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DEFINITION
ACCESSION
VERSION
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Best Local Similarity
Matches 430; Conserv
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/mol_type="mRNA"
/db xref="taxon:7739"
/clone="MMPMGP498A1518"
/tissue_type="whole embryo"
/dev_stage="5-6 hrs (gastrula stage)"
/lab_host="E.coli, XLI blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGP498)"
/note="Vector: pSport1; Site 1: SalI, KpnI, EcoRI (5');
Site_2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a SalI 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
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0; Mismatches 181
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                                        Homo
                                        sapiens cDNA,
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Matches 313; Conserv
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1 (bases 1 to 470)

Dias Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Roldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=IL&t2=IL-BT109-002.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST.
Homo sapiens (human)
Homo sapiens
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ACCGCGAGTGGGACCTGCTGAAGTACCGCTCCTTCGGCTATGGCCACTCCTTCGGCGTGC
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                                                         TGAAACTGGTGCGCCCCGGCATGCGCTGCAGCGATATCGCTCGGGAACTGAACGAGATCT
                                                                                  TIGCTTCCCGATGATCGCCGGCATATTACACCGCGTTGGAGCGCACGCTGTTCCTCGACC
                                                                                                                                                                                                                                                                                                                                                                                           GTTCCCCTTCGTGGAGCTGATGGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGA
                                                                                                                                  <u>ACTGCCCGGACGAGTACCTACGCCTGTGGCAGGCCAACGTCGAAGTGCACGAAGCCGGGC</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer: puc 18 forward.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 221; DB 1; Lo
Pred. No. 3.2e-38;
0; Mismatches 137;
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01509-010,

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Paulo-SP,

with

ORF

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470;

Indels

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Gaps

689

396

749

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                                                                                      ORIGIN
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. CDNA
clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Max-Planck-Institut fuer Molekulare Innestr.63-73, D-14195 Berlin, Germa Tel: +49 30 8413 1235
Email: poustka@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus purpuratus cDNA MPMGp69100990;MPI_SURUDI_90E9 5', m CD307119.1 GI:34752168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Bereinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H. Generation, annotation, evolutionary analysis, and database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD307119
494 bp mRNA linear EST StrPu691.009486 Sea urchin larva CDNA library MPMGp691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP) 5'-seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database of the German Human Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Poustka AJ
laboraty 145, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 494.
Location/Qualifiers
                                                                                                     /tissue_type="whole larva"
/dev stage="larva 2-3 weeks"
/lab host="E coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/note="Vector: pSportl; Site_1: NotI; Site_2: Sall; Random primed and directionally cloned in pSportl vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                         /clone="MPMGp691E0990;MPI_SURUDI_90E9"
17.1%;
66.8%;
Score 207.8; DB 6; Pred. No. 2.6e-35;
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                        Length 494
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CD295681
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procedure, clones that display the same hybridisation matrix with a battery of 200 mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                            Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
laboraty 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Tinnestr.63-73, D-14195 Berlin, Germany
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StrPu691.007076 Sea urchin larva cDNA library MPMCp691
                                                                                                                                                                                                                                                                                                 Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
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CD295681.1 GI:34746758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCCTTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 442)
                                                                                                                                                                                                                         il: poustka@molgen.mpg.de
library was characterised by oligonucleotide fingerprinting
F) to reduce sequencing redundancy. According to the ONF
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Best Local Sim
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                                                         AUTHORS
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CD296311
                                                                                             Strongylocentrotus purpuratus Strongylocentrotus purpuratus Entongylocentrotus purpuratus Eukaryota, Metazoa, Echinodermata; Eleutherozoa; Echinoidea; Echinoidea; Echinoidea; Echinoida; Strongylocentrotus.
1 (bases 1 to 519)
Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Camero Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach, Generation, annotation, evolutionary analysis, and
                                                                                                                                                                                                                                                        CD296311.1
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/tissue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab_host="E.coli, XL1 blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/note="Vector: pSportl; Site 1: Not1; Site 2: SalI; Random primed and directionally cloned in pSportl-Vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a SalI 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
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Pred. No. 4.4e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    procedure, clones that display the same hybridisation matrix with a battery of 200 Bmer oligonuclectices are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (http://www.rzpd.de) PCR PRImers
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Contact: Poustka AJ
laboraty 145, dept.Lehrach
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BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3'
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' psport3/8'
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Fax: +49 30 8413 1128
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The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
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          CGCATCGGCATCGAGTTCGACCACGTCAATCTCGACTTCCGCCGCCAGCTCGAGGAAGCC
                                                    GATTGGCATCGCGACAACTTCTGGAGCGCCGTTCGGCACCTGCTCGGCAACGCTTCGGNG
                                                                           GACTGGCGCCGCGACAATTTCTATCGCGCCGT---GCGCCAGCTGACCACGGGCGCCAAG
                                                                                                                               GTCGACAGCGGCCAGGCCTGGCGGAGATCACCCGTGAGCGACGATGTGGTCATCTACACG
                                                                                                                                                           ATCGACGGCCGGCCAGCCTGGCG------CCGCAGCTTCGGCGACAACATCACCTACACC 303
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/mol_type="mRNA"
/db_xref="taxon:7668"
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Pred. No. 8.9e-17;
0; Mismatches 208;
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Max-Planck-Institut fuer Molekulare Genetik
Thnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Tel: +49 30 8413 1235
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
all clones assigned to the same fingerprint cluster as the clone
from which the above EST is generated is available at the amphioxus
project site at http://www.molgen.mpg.de/amphioxus.
Clones and filters are distributed via the Resource Center/Primary
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CF919042
                                                                                                                                                                                                                                                                                                                                                        FORMARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAGGGGGATGTG 3' INsert Length: 1200 Std Error: 200.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database of the German Genome Project (http://www.rzpd.de).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Panopoulou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 13 (6A), 1056-1066 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRimers
                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 551.
/clone="MPMGp531L07115;BFL26_115L7"
                                                                                                                                                                                                                 /strain="wild type"
/db_xref="taxon:7739"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                     mol_type="mRNA"
                                                                                                                                                                                                                                                                           organism="Branchiostoma"
                                                                                                                                                                                                                                                                               floridae"
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148; Conserv
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laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
                       FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3'
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3'
                                                                PCR PRimers
                                                                                                                                                                                                                                                                                                                                                        Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Branchiostoma floridae
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22683279
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286 TGGÁCATGCÁTAACGGGCAGAAGGTCAAACCGACCTTCTCAGTGGAGGAACTCCAGAGAA 345
GGCTGGTCGTCACCATGGACAAAGTGCTCTTCTTATCCCCCAGCCGTTGACGGTGGTCAGC
                                                         CTTATCACTGCATCAACTACTATTCCGGCTGGCTGTACTGCTATTTCGGACGCAAGTACG
                                                                                                                                                                                                                                       GGCTGGACAAGCTGCGTGCTCATGCTCAGCAGCAGTAATATAGATGCAGCTCTCTTCACTT 405
                                                                                                                                                                                                                                                                                GCCAAAACGACGTTCGCGGCTGGATGGCCAAGAACAATGTCGATGCGGCGCCTGTTCACCT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 83.2; DB 7;
Pred. No. 6.9e-08;
0; Mismatches 108;
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525 265 465 205

BFL26 002560 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMGp531) Branchiostoma floridae cDNA clone MPMGp531L07115 5', mRNA 553 bp mRNA linear EST 26-AUG-2003

Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J., Herwig,R., Vingron,M. and Lehrach,H.

New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed animal

Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de) (M13RSP)

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TITLE
JOURNAL
COMMENT
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AUTHORS
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VERSION
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BZ894814
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Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148;
                                     Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
Class: shotgun.
                                                                                                                                                                                                                                                                                                         BZ894814
Hg4_0102 Hg pUC18 Library
genomic survey sequence.
BZ894814
                                                                                                                                     Unpublished (2 Contact: Goo Y
                                                                                                                                                                                                                                  Halobaculum gomorrense
Archaea; Euryarchaeota; Halobacteria;
                                                                                                                                                                                                                                                               Halobaculum gomorrense
                                                                                                                                                                                                                                                                                            BZ894814.1
                                                                                                                                                                            Goo,Y., Roach,J., Glusman,G.,
DasSarma,S., Ng,W.V. and Hood,
                                                                               Institute for Systems Biology
1441 North 34th Street, Seattle,
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                  Low-pass Sequencing for Microbial Unpublished (2003)
                                                                                                                                                                                                                       Halobacteriaceae; Halobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%;
Similarity 57.8%;
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                                                                                                                                                                                                         (bases 1 to 524)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole embryo"
/dev_stage="26 hrs (neurala stage)"
/lab host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
/rote="Vector: pSport1 (Gibco BRL); Site_1: Sall, KpnI,
/note="Vector: pSport1 (Gibco BRL); Site_1: Sall, KpnI,
EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT
primed and directionally cloned in pSport1 vector using a
NotI (5'-pSACTAGTTCTGARTCCGGACCGCCCCCC (T)15-3' and a
Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
/organism="Halobaculum
                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                             GI:33345290
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Pred. No. 6.9e-08;
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/ Halobaculum
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gomorrense"
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                                                                                                                                                                                                                                                                                                                                                   linear
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Matches 177
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zh Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, Large-scale identification of ESTs involved in the between rice and Magnaporthe grisea Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB656525
OSJNEc10P11.f OSJNEc Oryza sativa (japonica clone OSJNEc10P11 5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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CB656525
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University of Arizona
Biological Sciences W
                                                                                              BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: P column: 11
                                                                                                                                                                                                                                                                                                                      Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:
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                                                                                                                                                                                            FORWARD: gta aaa cga cgg cca gtg
                                                                                                                                                                                                                                  PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rhartoideae; Oryzeae; Oryza.
(bases 1 to 722)
                                               primer: gta aaa cga
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                                                                                                                                                                                                                                                                       http://genome.arizona.edu
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/strain="ATCC 700876"
/db_xref="rtaxon:43928"
/clone_lib="Hg_pUC18_Library"
/note="Vector: pUC18; Site_1: Smal; A shotgun library was
/note="Tuctof from Halbaculum gomorrense genomic DNA using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rod Wing
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Location/Qualifiers
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organism="Oryza sativa (japonica cultivar-group)"

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RESULT 10
CB683938
LOCUS
               REFERENCE
AUTHORS
                                                                                 SOURCE
ORGANISM
                                                                                                                           ACCESSION
VERSION
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Matches 260;
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                                                                                                                                       clone OSC
CB683938
                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                  CB683938 722 bp mRNA linear EST 09-OSJNEf12P21.f OSJNEf Oryza sativa (japonica cultivar-group) clone OSJNEf12P21 5', mRNA sequence.
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zh
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,
                                                                                                                           CB683938.1
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                            (bases 1 to 722)
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/note="Vector: pBluescript II I
XhoI; 6 hrs after innoculation
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/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10P11"
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45.0%;
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Pred. No. 8.5e-05;
0; Mismatches 318
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Rice_Blast (C9240-1)"
    Zhou, B.,
ng, G.
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BACKWARD: gga aac agc tat gac
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Location/Qualifiers
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Fax: 520 621 9288
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University of Arizona
Biological Sciences We
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Contact: Rod Wing
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                                                       ACCGACGTGCCGACGTACGTGATGTTCTACGACGAGCAAGCGGCGAACTACCCGGGCGGC
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/dev stage="3 week"
/lab_host="DH10B"
/clone_libb="0SJNEf"
/note="Vector: pBluescript I
XhoI; Uninfected Control"
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be conditioned. Data and cathory (Qualifiers)
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ALOS3013
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|db_xref="taxon:7227"
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71; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      venuprante, a major partnership french Unpublished (2003)
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1 (bases 1 to 712)
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    GGCCACTCCTTCGGCGTGCTGCCACTACTACGGTCGCGAGGCCGGCGTGGAGCTGCGC 1029
                                                                                                                                              CAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATCGTGCAATCC
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                                      TCCGGCTCCCTGCCCCTCAGCGCGCTCCTGCTCGCCGCGCGCCACATGCCCGACGCGGCC
                                                                             ATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCCTTCGGCTAT 969
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/tissue_type="root"
/clone_lib="AZO2"
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/cultivar="recital"
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Best Local Sim
Matches 185;
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                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB659172 812 bp mRNA COUNTECTSO18.f OSJNEC OTYZA SATIVA (japonica Clone OSJNEC15018 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: gta aaa cga cgg cca gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: gta aaa cga cgg cca g
BACKWARD: gga aac agc tat gac
Plate: 15 row: O column: 18
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazu Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 812)
Jantasuriyarat, C., Lu, G.,
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                                                      CCCGAGCATGAAGTGGCGATCGCCACCACCAATGCGATGATCCGCGAGATCGCCAAATCG
                                                                                                                         GGAGACGGCGGCGGTGGCGGCGTCGGGAGCTGGGCGACGTTCTTGCAGCACGCCTG
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                             /clone_lib="OSJNEc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site.
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1
                                                                                                                                                                                                                                                                                                                                  /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/mol_type="mRNA"
/cultivar="Nipponbare"
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/clone="OSJNEc15018"
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47.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 604)
Sasaki, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305-8602, Japan
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                           GCGCACAATCCGGTCACCAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACC
                                                                                                                                                                                                                            CCCTTCGTGGAGCTGATGGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGACGGC
                                                        CTCTACTGGATGGGCGGCCTCGACCCGCGCCCTTGGCCCCTTCCTCCTCCTCCTCGTC
                                                                                     TTCCCGATGATCTTCGGCTACTACACCGCGCGCTGGAGCGACGCTGTTCTGCGACCATGTC
                                                                                                                           GCGCGCÁCCGCCGGCCGACCTACCCÁTGGAGCTCGCCCTCCCCÁCCGCCTTCGTCGTCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGTGCTCAGCCGCGTGACCAAGTCCGACGTGAAGCGGCTCGTCCGCGACCTCGAGTCC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA from mature leaf (2000)
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                /tissue_type="mature leaf"
/clone_lib="Rice mature leaf"
                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:39947"
/clone="S21656"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 0.0065;
Mismatches 285;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science, plant material and RNA prepared at Texas A & M University, sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences over the sequences are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA CLONE CCCI_37_H01_A007 Callus culture/cell suspension Sorghum bicolor CDNA Clone CCCI_37_H01_A007 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Rathore,K.,
Eastman,A. and Pratt,L.H.
An EST database from Sorghum: callus culture and cell suspension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                                  Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: CCC1_37_H01.b1_A007
Contact: Cordonnier-Pratt MM
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Other_ESTs: CCC1_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCGGCGGCGGCGCGCGCTGCCTCGTCGCCGACTTCCCGGCCATCAAGGCCGTCGGG 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        706 542 1860
706 583 0210
                       /db_xref="taxon:4558"
/clone="CCC1 37 H01 A007"
/lab_host="DH108-T1 phage-resistant E. coli"
/clone_lib="C2llus culture/cell suspension"
/clone_lib="C2llus culture/cell suspension"
/note="Vector: pME18S-FL3; Site_1: XhoI; kite_2: XhoI;
library was prepared from a mixture of polyA+ RNA from callus culture tissue and cells in suspension culture.
Double-stranded_CDNA was cloned_unidirectionally_into
different DraIII sites of the pME18S-FL3 vector (5-prime
                                                                                                                                                                                                                                                           cultivar="RTx430"
                                                                                                                                                                                                                                                                                                                organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                        type="mRNA
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                                                                                                                                                                                                                                                                                                                                                        CGGCTGGCTGTACTGCTATTTCGGACGCAAGTACGGCATGGTCATCGACCACAACAACGC
                                                    CAACCACAACGCCGACTCCGGCCGGGACTTCACCTGAGTGCAGGCGCTCGGCGTCACCTT
                                                                              CACCATCAAGTCGCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCGCGTGTGTGACGT
                                                                                                         GGACGAGAGCTTCTGCCTCGTCTCCGACGACCGCCTCCACATCAACGCGCGGTTCATGGG
                                                                                                                                                              GTGCGGCGACCCGCGGTTCACGGGCGCCGACGGCAACACCTTCTACTTCCACGGCAAGAA
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nilarity 47.5%;
Conservative
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Search completed: November 19, Job time: 4241 secs 2004, 19:22:01

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 s
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length: 2000000000
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
    4134886 seqs, 2624710521 residues
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Copyright (c) 1993 - 2004
geneseqn2003cs:*
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9743.183 Million cell updates/sec
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Score	Query Match	Length	BG	ID	scriptio
	99.9	1212	20		Aat61367 Cr
1210.4	99.9	1212	N	AAT38807	Aat38807 Cr
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17 635.6 18 634 19 563 20 456.2	6.5	63			16 640.	973	14 975.	976	976	976	10 978.	9 981.	8 981.	7 1184.	6 1210.	5 1210.	4 1210.	3 1210.	2 1210.	1 1210.	Result No. Score
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DANKED	Aan90635	Aan70877	Aan81271	Aan60274	Aat05502	Acc69520	Acc69521	Acc69518	Acc69516	Acc69517	Acc69515	Acc69519	Acc69514	Aat13291	Aba93696	Aai99856	Aas14742	Aav35699	Aat38807	Aat61367	Description
	-	Sequence	. Sequence	Sequence		_	Mutant Er	Mutant Er	Mutant Er	Mutant Er	Mutant Er	Mutant Er	Erwinia s	Creatine		5 Alkaligen	2 Creatine	Stable cr	7 Creatine	Crea	ion

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AAH74537	AAZ06824	ABK91624	ADJ39271	ADN40876	AAQ52638	AAD46285	ABV74978	AAV08896	ACA23861	AAA50948	ACC44573	ABA03041_18	ACA36793	ABL61294	AAD17186	AAD17184	ABQ44817	ABQ44816	ADG73352	ADG73350	ABD05710	ABD05831	ABD05567
Aah74537 Nucleotid	Aaz06824 Streptomy	Abk91624 Modified		Adn40876 Plasmid p	Aaq52638 Streptomy		Abv74978 Synthetic	Aav08896 Cellobios	Aca23861 Prokaryot	Aaa50948 Humanised	Acc44573 Glucoamyl	Continuation (19 o	Aca36793 Prokaryot	Abl61294 N. unifor	Aad17186 Streptomy	Aad17184 Streptomy	Abq44817 Oligonucl	Abq44816 Oligonucl	Adg73352 Pseudomon	Adg73350 Pseudomon	Abd05710 Pseudomon	Abd05831 Pseudomon	Abd05567 Pseudomon

ALIGNMENTS

RESULT 1 AAT61367 Thermal stability; creatinine amidinohydrolase; creatine; sarcosine; urea; blood; ds. 16-MAY-1995; Creatinine amidinohydrolase coding sequence 17-APR-1997 16-MAY-1995; 26-NOV-1996. JP08308579-A. Alcaligenes faecalis. AAT61367; AAT61367 standard; DNA; 1212 BP. (first entry) 95JP-00117283 95JP-00117283

Gene coding for creatinine amidinohydrolase - used to quantify blood or urinary creatinine as a disease indicator.

P-PSDB; AAW11861.

WPI; 1997-059698/06. (тоум) тоуово кк.

Claim 4; Page 10-11; 12pp; Japanese.

which has a low Km value for creatine. The creatinine amidinohydrolase has the following physicochemical properties: (a) action: converts creatine and water into sarcosine and rourea; (b) optimum temp.: 40-45 deg.C; (c) optimum pH: 8.0-9.0; (d) thermal stability: about 50 or less (pH 7.5, 30 mins); (e) stable pH: a Ph range of about 4-10; (f) Km value: about 15.2 mM; (g) mol. wt.: about 4300 (SDS-PAGE); and (h) isoelectric point: about 3.5. The creatinine amidinohydrolase may be used in the quantification of blood or urinary creatinine and creatine as an indicator of various diseases This sequence encodes a thermally stable creatinine amidinohydrolase

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A novel creatine amidinohydrolase enzyme has been developed which catalyees the reaction of creatine with water to form sarcosine and urea, is stable at temperatures of up to 50 degrees Celsius (pH 7.5, 30 minutes) and has an optimum temperature of 40-50 degrees Celsius, optimum pH of 8-9, a Km value for creatine of 3.5-10 mM in a binding assay using sarcosine oxidase and peroxidase, a molecular weight of 43 kD by SDS-PAGE and an isoelectric point of 3.5. The present sequence encodes creatine amidinohydrolase derived from Alcaligenes faecalis strain TE3581 (FERM P-14237), which is the wild type creatine amidinohydrolase to be mutated in the present invention. The enzyme can be used to determine creatine in a sample by measuring the absorbance of a dye formed by reacting the sample with a reagent, comprising the enzyme, sarcosine oxidase and a composition for detecting hydrogen peroxide, e.g. for diagnosis of

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P-PSDB; AAW22893.
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Best Local Sim
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                                                                                                                                            GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACACCC
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Query Match
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                                                                                             This DNA encodes a stable creatine amidinohydrase which is a mutant creatine amidinohydrase and has improved long-term stability in a ne buffer compared to wild type creatine amidinohydrase. A recombinant plasmid containing the stable creatine amidinohydrase gene can be us transform a cell for the recombinant production of the enzyme. This stable creatine amidinohydrase is useful as a diagnostic agent can be produced commercially
                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-421167/36.
P-PSDB; AAW61905.
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The invention relates to Alcaligenes faecalis creatine amidinohydrolase, which catalyses creatine and water to sarcosine and urea. Creatine amidinohydrolase can be produced by culturing a microorganism producing the protein in a nutrient medium and recovering the protein from the resulting culture. Creatine amidinohydrolase is useful as a routine reagent for clinical tests for determining creatine and creatinine in biological samples. This is particularly useful in diagnosing diseases such as uraemia, chronic nephritis, acute nephritis, giantism and tonic muscular dystrophy. The presence of creatine in a sample can be determined by measuring an absorbance of a pigment produced by the reaction of a reagent containing creatine amidinohydrolase with the sample. This sequence represents genomic DNA encoding Alcaligenes

Disclosure; Page 15-16; 21pp; English

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Query Match
Best Local Simi
Matches 1211;
                                       Sequence 1212 BP; 244 A; 400 C; 358 G; 210
                                                         The invention relates to Alcaligenes faecalis TE3581 (FERM P-14237) creatineamidinohydrolase and the encoding gene. The gene can be used the commercial preparation of creatineamidinohydrolase. (Updated on 0 AUG-2003 to correct OS field.)
                                                                                                                                               WPI; 2002-003140/01.
P-PSDB; AAM51471.
                                                                                                                                                                                                                                                                                                                                                          Alcaligenes faecalis.
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                                                                                                         Claim 4; Page 10; 11pp; Japanese.
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                                                                                                                                                   The present invention describes a stable mutant creatine amidinohydrase having a long-term stability in a neutral buffer solution. Also described are: (1) a creatine amidinohydrase gene encoding the above stable creatine amidinohydrase; (2) a gene encoding a mutant creatine amidinohydrase; (2) a gene encoding a mutant creatine compared to wild type creatine amidinohydrase, in which at least one gene among those found in a fully defined 1212 nucleotide sequence (the present sequence) is replaced by another gene; (3) a recombinant plasmid containing a gene encoding the above creatine amidinohydrase; (4) a cell transformed by the above plasmid; and (5) a method for the preparation of a stable creatine amidinohydrase in which the above cell is cultured in a medium and creatine amidinohydrase is collected. The creatine amidinohydrase is useful as a clinical diagnosing agent
                                                                                                              Sequence 1212
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term stability in a neutral buffer solution.
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Best Local S
Matches 1195
                                                                                                                                                                                                                                                                                                                                               CAH is used for quantification of creatine, e.g. to diagnose kidney disease by measuring creatine content of serum or urrine. CAH DNA can be inserted into host cells for the prodn. of CAH. CAH can now be produced efficiently without having to add creatine to the culture medium. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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Pred. No. 3.2e-191;
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Similarity

Conservative

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Score 981.6; DB 8; Pred. No. 6.5e-157; 0; Mismatches 144;

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242 A; 392 C; 81.0%;

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The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, IZ78, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. Also described is a reagent (II) for determining creatine comprising the Erwinia-type creatinase variant. The variant is useful for determining creatining and/or creatine concentration in a sample. Measuring creatinine and creatine are useful for diagnosing uraemia, chronic nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some other related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better suited to detection methods for creatine. The present sequence encodes Erwinia sp. (DSM 97-934) wild-type creatinase from the present invention
                                                                                                                                                                                                                                                                                                                     New variant of an Erwinia-type creatinase modified relative to a wild-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.
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                                                                                                                                                                                                                                                                                            Disclosure; Page 15-17; 51pp; English
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                                                                             The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. Also described is a reagent (II) for determining creatine amidinohydrolase. Erwinia-type creatinase variant. The variant is useful for determining creatinine and/or creatine are useful for dagnosing uraemia, chronic creatinine and creatine are useful for dagnosing uraemia, chronic creatinine, acute nephritis, gigantism, tonic muscular dystrophy and some other related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better without for diseases. The mutant enzymes have improved atability, lower suited to detection methods for creatine. The present sequence encodes a
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creatinine and/or creatine concentration in a sample.
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New variant of an Erwinia-type creatinase modified relative to a wild-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.

Example 4; Page 20-21; 51pp; English.

The present invention describes a variant of an Erwinia-type creatinase CC (I) modified relative to a wild-type creatinase having creatinase CC activity. The variant comprises at least one amino acid substitution at a CC position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, 1278, 11304 and F395. Creatinase has CC the EC number EC 3.5.3.3 and is also known as creatine comprising the EC Also described is a reagent (II) for determining creatine comprising the CC Erwinia-type creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and creatine are useful for diagnosing uraemia, chronic CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some CC conductivity and/or lower Mervalues for creatine: they are much better CC suited to detection methods for creatine. The present sequence encodes a CC mutant Erwinia creatinase from the present invention

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                                               GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
                                                                               AAGAACGTCGCCGTGCACCGCCGCGGCCTCGAACTCATCAAGCCGGGTGCGCGCTGCAAG
                                                                                              GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG
                                                                                                                                                                         GTGCAATCGGGCGATATCCTGTCGCTCAACACGTTCCCGATGATCTTCGGCTACTACACG
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88.0%;
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2.2e-156;
nes 146;
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RESULT 11

ACC69517

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                                                                                                                                                                                                          New variant of an Erwinia-type creatinase modified re
type creatinase having creatinase activity, useful fo
creatinine and/or creatine concentration in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3
Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism;
chronic nephritis; acute nephritis; tonic muscular dystrophy; muta
                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                               (HOFF
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HOFFMANN LA ROCHE
                                                                                                                                                                                                                                                                                                                                                                                Schmuck R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGTCGGGGAGGACGGTGCCGAGAACATCACCGGCTTCCCGTTCGGTCCGGAACACACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGTGATGTTGCCAGAAGGCGCTCCCGGCGCGCGGGGGCTACCGCGAGCACGACATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/partial
/EC_number= "3.5.3.3"
/product= "creatinase mutant
/note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant;
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The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.

Example

4.

Page 26-28;

51pp;

English.

886666666666666

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Query Match
Best Local Simi
Matches 1065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1212 BP; 240 A; 394 C; 358 G; 220 T; 0 U; 0 Other;
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GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG
                                                                                                                                            GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACC
                                                                                                                                                                                                     ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCCCACAATCCGGTGACCAACCGCATC
                                                                                                                                                                                                                          ACCTGGTTCCAGTCGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATC
                                                                                                                                                                                                                                                                                                                      AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAGCTGATGGACACCTGG
                                                                                                                                                                                                                                                                                                                                                                GCTGCGTTGCCGCCGTCAAGGCCGGCGTTCCGGAGCACCAGGGTCGCGATCGCCACCAACC
                                                                                                                                                                                                                                                                                                                                                                                                         GCCTGCGCGGCTGCCATCAAGGCCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCGCTCGAAGAAGCAGAAGCTGATCCGCGAGGGTGCCCGTATCTGCGACGTCGGCGGTGCC
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                                      GCGCTGGAGCGAACGCTGTTCTGTGACCACGTCGACGATGCCAGCCTTGACACCTGGGAG
                                                                                                                    GTGCAATCGGGCGATATCCTGTCGCTCAACACGTTCCCGATGATCTTCGGCTACTACACG
                                                                                                                                                                                                                                                                                  AATGCGATGGTCCGCGAGATCGCCAAGTCGTTCCCCCTTCGTCGAACTGATGGACACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCCCGGCGTCGAGTTCGTCGATATCGGTCAACCGTCGATGTGGATGCGCACGGTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.6%;
milarity 87.9%;
Conservative
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Pred. No. 4.2e-156;
0; Mismatches 147;
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New variant of an Erwinia-type creatinase modified relative to type creatinase having creatinase activity, useful for determing creatinine and/or creatine concentration in a sample.

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                                                                                   WPI; 2003-383834/37.
P-PSDB; ABR43475.
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The present invention describes a variant of an Erwinia-type creatinase CC (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has CC these are selected from N130, M203, I278, I1304 and F395. Creatinase has CC these creatine EC 3.5.3.3 and is also known as creatine amidinohydrolase. CC Also described is a reagent (II) for determining creatine comprising the Erwinia-type creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and/or creatine are useful for diagnosing uraemia, chronic nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some CC orber related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better suited to detection methods for creatine. The present sequence encodes a cut of the conductivity and creatinase from the present invention
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Erwinia sp. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant Erwinia creatinase CT2m28 encoding DNA SEQ
                                                                                                             17-SEP-2002;
                                                                                                                                                                             EP1298213-A1
                                                                            20-SEP-2001;
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                                                                                                                                                                                                          /*tag= a
/EC_number= "3.5.3.3"
/product= "creatinase
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CC The present invention describes a variant of an Erwinia-type creatinase CC (I) modified relative to a wild-type creatinase having creatinase CC activity. The variant comprises at least one amino acid substitution at a CC position of the fully defined 404 amino acid sequence given in ABR43467; CC these are selected from N130, M203, I778, I1304 and F395. Creatinase has CT these creatine EC 3.5.3.3 and is also known as creatine amidinohydrolase. CC Also described is a reagent (II) for determining creatine comprising the CC Erwinia-type creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and creatine are useful for diagnosing uraemia, chronic CC comparists, acute nephritis, gigantism, tonic muscular dystrophy and some CC conductivity and/or lower Km-values for creatine; they are much better suited to detection methods for creatine. The present sequence encodes a CC mutant Erwinia creatinase from the present invention
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Best Local S
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P-PSDB; ABR43477.
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                                                   GCCTGCGCGGCTGCCAACGACCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCACC
AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAGCTGATGGACACCTGG
                               GCCTGCGTTGCCGCCGTCAAGGCCGGCGTTCCGGAGCACGAGGTCGCGATCGCCACAACC
                                                                                                    TCGCTCGAAGAGCAGAAGCTGATCCGCGAGGGTGCCCGTATCTGCGACGTCGGCGGTGCC
                                                                                                                      TCGCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCCGCGTGTGTGACGTCGGCGCGCG
                                                                                                                                                                      CTGCCCGGCGTCGAGTTCGTCGATATCGGTCAACCGTCGATGTGGATGCGCACGGTCAAG
                                                                                                                                                                                         CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAG
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                                                                                                      Brwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3 Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism; chronic nephritis; acute nephritis; tonic muscular dystrophy; muta
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Schmuck R,
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Search completed: November 19, 2004, 16:39:00 Job time : 664 secs

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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ALIGNMENTS

NAME: ROBERT F. Green REGISTRATION NUMBER: 7855 REFERENCE/DOCKET NUMBER: 7806 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 616-5600 TELERAX: (312) 616-5700 TELEX: 25-353 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1212 base pairs TYPE: nucleic acid companyments of child SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/799,897 FILING DATE: 11-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UMBER: UP 25435/1996 FILING DATE: 13-FEB-1996 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Application US/08799897 RE: LEYDIG, VOIT & MAYER, LTD. Two Prudential Plaza, Suite 4900 : Alcaligenes faecalis TE3581 (FERM P-14237) Hattori, Takashi Nishiya, Yoshiaki Kawamura, Yoshihisa TVENTION: NOVEL CREATINE AMIDINOHYDROLASE, PRODUCTION Sogabe, Atsushi genomic DNA 27555 78064

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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Alca
STRAIN: FERM B
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CITY: New York
STATE: New York
COUNTRY: USA
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FERM BP-4487
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APPLICATION NUMBER: US/08/947,726A
FILING DATE: 09-OCT-1997
CLASSIPICATION 235
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,444
FILING DATE: 27-SEP-1995
PRIOR APPLICATION NUMBER: US 08/535,444
FILING DATE: 27-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 94/235737
FILING DATE: 29-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence III, Stanton T.
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-120-995
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 790-9090
TELEPAN: (212) 869-9741
                                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
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APPLICANT: Ichikawa, Toshio
APPLICANT: Suzuki, Marsaru
APPLICANT: Koyama, Yasuji
TITLE OF INVENTION: A NOVEL CREATINE AMIDINOHYDROLASE GENE,
TITLE OF INVENTION: A NOVEL RECOMBINANT DNA, AND A PROCESS
TITLE OF INVENTION: CREATINE AMIDINOHYDROLASE
NUMBER OF SEQUENCES: 5
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                             TYPE: nucleic acid
STRANDEDNESS: doub
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                                                  GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
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                                                                                                   AAGAACGTGGCCGTGCATCGCCGCGCGCGCTGCAAG
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Pred. No. 1.3e-253;
0; Mismatches 5;
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APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO P
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4171
LENGTH: 858
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4171
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Best Local Similarity
Matches 316; Conserv
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  GCGCTGCAAGGACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAA
                         CCTCTGCCAGATCACCCAGGAATGCATGTACAAGGGCATTTCCGTGGTGCGTCCGGGCGC
                                                CATCTGGGAGAAGAACGTGGCCGTGCATCGCCGCGGGCTCGAGCTGATCAAGCCGGGCGC
                                                                         CTACCACGGCGACACCAGCAAGATGTTCCTGGTCGGCAAGACCCCGGAATGGGCCGACCG
                                                                                           CTACTACACGCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGA
                                                                                                                         CAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGG
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nilarity 46.3%;
Conservative 0
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APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO F
ITITE OF INVENTION: AUGUSTICS ACID AND AMINO ACID SEQUENCES RELATING TO F
ITITE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 435
LENGTH: 963
TYPE: DNA
TYPE: DNA
TYPE: DNA
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US-09-22-991A-4435/c
; Sequence 4435, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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US-09-252-991A-4435
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  CCTCTGCCAGATCACCCAGGAATGCATGTACAAGGGCATTTCCGTGGTGCGTCCGGGCGC
                                    CATCTGGGAGAAGAACGTGGCCGTGCATCGCCGCGGGCTCGAGCTGATCAAGCCGGGCGC
                                                                          CTACCACGGCGACACCAGCAAGATGTTCCTGGTCGGCAAGACCCCCGGAATGGGCCGACCG
                                                                                                              CTACTACACCGCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGA
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Pred. No. 2.5e-07;
0; Mismatches 360
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4314
LENGTH: 1176
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US-09-252-991A-4314
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Best Local Simi
Matches 316;
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APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ESEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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                                                                                                                  CGAGAAGCCGCTGAAGGAAGGCGACATCCTCAACGTCGACATCACCGTCATCAAGGACGG
                                                                                                                                                ÇAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGG
                                                                                                                                                                                          GGGCTTTCCCAAGTCGATCTGCACCTCGATCAACCATGTGGTCTGCCATGGCATCCCCAA
                                                                                                                                                                                                                             GGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCAC
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Pred. No. 2.6e-07;
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RESULT 6
US-08-939-002A-1
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 221193/1997
APPLICATION NUMBER: JP 221193/1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 8361-001-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: HAYASHI
APPLICANT: LIU, AII
APPLICANT: LI, HEE
APPLICANT: HARAGUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08939002A Patent No. 5849529
                                                                                                                TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LI, HEBIAO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: KITAMURA, YOSHIAKI
TITLE OF INVENTION: CELLOBIOSE PHOSPHORYLASE GENE, VECTOR
TITLE OF INVENTION: AND TRANSFORMANT CONTAINING SAID GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, ADDRESSEE: P.C.
                                                   TOPOLOGY:
                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/939,002A
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Best Local Similarity
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LOCATION: 359..2824
OTHER INFORMATION: /note= "METHOD
OTHER INFORMATION: SEQUENCE: E"
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Pred. No. 3.3e-05;
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RESULT 7
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APPLICANT: Nakamu
                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
                                                                                                                                                                  MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Haley, Jr., James F.

REGISTRATION NUMBER: 27794
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: SI
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          IDENTIFICATION P
                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                 STRANDEDNESS:
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FILING DATE: 19-MAY-1992
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                                                                            LOCATION: 359..364
IDENTIFICATION METHOD:
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Tsuzuki, Hiroshige
Kitadokoro, Kengo
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Sequence 2, Application US/09025691
Patent No. 6069299
GENERAL INFORMATION:
APPLICANT: Broadway, Roxanne M.
APPLICANT: Harman, Gary E.
APPLICANT: Harman, Gary B.
TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
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Best Local Similarity
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IDENTIFICATION METHOD:
NAME/KEY: 81g peptide
LOCATION: 435..944
IDENTIFICATION METHOD:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:

99-025-67
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Matches 389;
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Best Local (
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE: CHARACTERISTIS:
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NAME: GOIdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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CITY: New York
"TATE: New York
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ADDRESSEE: Nixon, Hargrave, E
STREET: Clinton Square, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
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Similarity 42.5%;
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                           GCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACCGC
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Pred. No. 9.1e-05;
0; Mismatches 523;
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. Box 1051
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APPLICANT: LIAN, Ying
APPLICANT: HARTOG, KARIN
APPLICANT: HARTOG, KARIN
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POI
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION MUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
LENGTH: 1599
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Best Local :
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Patent No. 6602
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APPLICANT: SRIVASTAVA, Indresh
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                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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AGCTGGGAGAAGATGCCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGC
                               GACAATTTCTATCGCGCCGTGCGCCAGCT---GACCACGGGCGCCAAGCGCATCGGCATC
                                                                                                      GGCGGCCAGCCCTGGCGCAGCTTCGGCGACAACATCACCTACACCGACTGGCGCCGC
                                                                                                                                        CCCCTGTGCGTGACCCTGAACTGCACCGACAAGCTGACCGGCAGCACCAACGGCACCAAC
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                                                                   AGCACCAGCGCACCAACAGCACCAGCGCACCAACAGCACCAGCACCAACAGCACCGAC
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                                                                                                                                                                                                             Score 60.6; DB 4;
Pred. No. 0.00023;
0; Mismatches 579;
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APPLICANT: BARNETT, SUBAN
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF
                                                                                                                                                                                                                                                                RESULT 10
US-09-475-515-56
                                                                                                                                                                                                    Sequence 56, Applicat Patent No. 6602705 GENERAL INFORMATION:
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FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 56
LENGTH: 2112
TYPE: DNA
ORGANISM: Artificial Sequence
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34; Conservative
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                                           CACTCCTTCGGCGTGCTGTGCCACTACTACGGTCGCGAGGCCGGCGTGGAGCTGCGCGAG
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APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
FILE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 2112
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COLUMN TRANSPORMETTON. DESCRIPTION of Artificial Sequence
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Patent No. 6602705
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
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 AGCTGGGAGAAGATGCCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGC
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                               TGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCCCGCCTTCGCC
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Pred. No. 0.00025;
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                                          GACGGTGCCGAGAACATCACCGGCTTCCCGTTCCGGTCCGGAACACCATCATCCGCAA 1211
                                                                                           AAGGAGAACGACCATCATCCTGCCCTGCCGCATCCGCCAGATCATCAACATGTGGCAG 1320
                                                                                                                                        CCGGAGGGCATGCCCGGTGCCGGCCGCTATCGCGAGCACCATCCTGATCGTCGGGGAG 1152
                                                                                                                                                                                       TGCAACACCAGCCAGCTGTTCAACAGCACCTGGAACATCACCGAGGAGGTGAACAAGACC 1260
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GAGGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGCGGCCAGATCAAGTGCAGCAGCAA 1379
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APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAW, Ying
APPLICANT: LIU, Hong
APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 2181
TYPE: DNA
ORGANIT: US-09-475-515-58 OTHER INFORMATION: Description of Artificial Sequence: gp140TM.modUS4 ORGANISM: Artificial Sequence FEATURE:

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                                                GACGGTGCCGAGAACATCACCGGCTTCCCGTTCGGTCCGGAACACCATCATCCGCAA 1211
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Pred. No. 0.00025;
0; Mismatches 579;
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIU, Hong
APPLICANT: HARTOG, Karin
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: OP VIRUS-LIKE PARTICLES
FILE OF INVENTION: OP VIRUS-LIKE PARTICLES
FILE REPERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 64
LENGTH: 2634
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COURTED INCOMMETTON: Description of Artificial Sequence
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; Sequence 64, Application
; Patent No. 6602705
; GENERAL INFORMATION:
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Best Local Similarity 42.6%;
Matches 434; Conservative
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ATCGTGCAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGT
                               GAÇATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACCGCGCTGGAGCGC
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Pred. No. 0.00026;
0; Mismatches 579;
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AGCTGGGAGAAGATGCCCGAGGGCGAGATCAAGAACTGCAGCTTCAACATCACCACCAGC

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APPLICANT: STAVA, Indresh
APPLICANT: STAVA, Indresh
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
APPLICANT: WALKER, Christopher
APPLICANT: HARTOG, MARK
APPLICANT: HARTOG, OF VIRUS-LIKE PARTICLES
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
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US-09-475-515-73
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Patent No. 6602705
                                                                                                                                                                                                                                                                         -09-475-515-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BARNETT,
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial OTHER INFORMATION: gp160.modUS4.gag.modSF2
                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 4766
                                                                                                                                                                                                                   Local Similarity
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Pred. No. 0.00029;
0; Mismatches 579
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                                                                                                                                                         Sequence 4, Application US/09025691 Patent No. 6069299
GENERAL INFORMATION:
                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                     APPLICANT: Broadway, Roxanne M.
APPLICANT: Harman, Gary E.
TITLE OF INVENTION: FUNCIS AND INSECT CONTROL
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
ADDRESSEE: Nixon, Hargri
STREET: Clinton Square,
CITY: Rochester
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                                 Hargrave,
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
ELENGTH: 2712 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
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Best Local Similarity 43.2%;
Matches 394; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION UMMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/20120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                          GAGTCGGTCGACGGCGTCGCCGACACCTGGGGACCAGCCGCTGCGCGGCAACTTCAACCAG
                                                                                AATCCGGTCACCAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCG
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Pred. No. 0.00043;
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Search completed: November 19, 2004, 14:49:17 Job time : 128 secs

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Perfect score:
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Match Length
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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Sequence 17, Appli
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Sequence 11, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 19, Appl
Sequence 88003, A
Sequence 109294,
Sequence 38426, A
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CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10251078 Publication No. US20030119084A1 GENERAL INFORMATION:
                                                                                                                          Matches 1068;
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type creatinase
FILE REFERENCE: 20981 EP
                                                                                                                                                                                                                                                                                     LENGTH: 1215
TYPE: DNA
ORGANISM: Erwinia sp.
                                                                                                                                            Match 81.0%;
Local Similarity 88.1%;
    61 TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC 120
                                                              ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG
                                             ATGACTGACGACATGTTGCACGTGATGAAATGGCACAATGGTGAGAAGGAATATTCCCCC
                                                                                                                          Conservative
                                                                                                                      Score 981.6; DB 15;
Pred. No. 8.9e-254;
0; Mismatches 144;
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                                                            ATGGTGATGCTGCCGGAGGGCATGCCCGGTGCCGGCGGCTATCGCGAGCACCGACATCCTG
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COGANISM: Artificial Sequence
FEATURE:
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                                            CTGCCCGGCGTCGAGTTCGTCGATATCGGTCAACCGTCGATGTGGATGCGCACGGTCAAG
                                                                                                   CGCATCGGTATCGAGTTCGATCACGTGGACCTTGACTTCCGCCGCACGCTCGAAGAGGCG
                                                                                                                                                                      ACCGACTGGCGCCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAG
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420 360 360 300

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240 180 180

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PILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/10251078
Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kratzsch, Peter
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type
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Score 981.6; DB 15;
Pred. No. 8.9e-254;
0; Mismatches 144;
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    Gaps
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RESULT 3
US-10-251-078-9

Sequence 9, Application US/10251078

Publication No. US20030119084A1

GENERAL INFORMATION:

APPLICANT: Roche Diagnostics GmbH

APPLICANT: Schmuck, Rainer

APPLICANT: Kratzsch, Peter

APPLICANT: Kratzsch, Peter

APPLICANT: Weisber, Harald

ITITE OF INVENTION: Variants of an Erwinia-type cre.

FILE REFERENCE: 20991 EP

CURRENT APPLICATION UMBER: US/10/251,078

CURRENT APPLICATION UMBER: US/10/251,078

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9
 LENGTH: 1215
TYPE: DNA
ORGANISM: Artificial S
FEATURE:
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US-10-251-078-9
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                                       GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG
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Pred. No. 6.5e-253;
0; Mismatches 146;
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; OTHER INFORMATION: Description: PEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1212)
US-10-251-078-11
                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10251078

Publication No. US20030119084A1

GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Schao, Zhixin
APPLICANT: Schao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-t
FILLE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 1212
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Best Local Similarity
Matches 1065; Conserv
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ORGANISM: Artificial
FEATURE:
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   TCGGCCGGCATCGATGGCGGTCAGCCTGGCGCGTAGCTTCGGCGACAACATCACCTAT
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                TCGGCCGGCATCGACGGCCGGCCAGCCTGGCGCCGCAGCTTCGGCGACAACATCACCTAC
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Pred. No. 1.7e-252;
O; Mismatches 147;
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RESULT 5
US-10-251-078-13
; Sequence 13, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
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; LOCATION: (1)..(1212)
US-10-251-078-13
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APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type creatinase
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
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Best Local Similarity 87.9%;
Matches 1065; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
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Pred. No. 1.7e-252;
0; Mismatches 147;
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TYPE: DNA

GRANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description:
FEATURE:
NAME/KEY: CDS
JCCATION: (1)...(1215)
US-10-251-078-15
                                                                                                                                                                        APPLICANT: Shao, Zhixin

APPLICANT: Schmuck, Rainer

APPLICANT: Kratzsch, Peter

APPLICANT: Kenklies, Janet

APPLICANT: Weisser, Harald

TITLE OF INVENTION: Variants of an Erwinia-t

FILE REFERENCE: 20981 EP

CURRENT APPLICATION NUMBER: US/10/251,078

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 1215
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Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
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                                 Score 976.8; DB 15;
pred. No. 1.7e-252;
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ATCGTCGGGGAGGACGGTGCCGAGAACATCACCGGCTTCCCGTTCGGTCCGGAACACACC 1200
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                                   ATGGTGATGTTGCCAGAAGGCGCTCCCGGCGCGCGGCGGCTACCGCGAGCACGACATCCTG
                                                      ATGGTGATGCTGCCGGAGGGCATGCCCGGTGCCGGCGCTATCGCGAGCACGACATCCTG
                                                                                                         GAACTGCGCGAGGACATCGATACCGTGCTGCAGCCCGGCATGGTGGTCTCCATGGAGCCG
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APPLICANT: Kratzsch, Peter
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-t
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1212
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
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Best Local Similarity 87.8%;
Matches 1064; Conservative
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APPLICANT:
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OTHER INFORMATION:
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                                          CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAG
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Pred. No. 4.7e-252;
0; Mismatches 148;
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Sequence 19. Application US/10251078
Publication No. US20030119084A1
Publication No. US20030119084A1
PUBLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Shao, Zhixin
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-t
PILS REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 1212
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LENGTH: 1212
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: [
; FEATURE:
; FAATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1212
US-10-251-078-19
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Best Local Similarity 87.7%;
Matches 1063; Conservative
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                                     ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG
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Pred. No. 1.3e-251;
0; Mismatches 149;
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660 720 720

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480 540 540 480

GATATCGCCATCGAACTCAACGAGATGTACCGGGAGTGGGATCTGCTGAAGTACCGCTCC

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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 88003
LENGTH: 2733
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
FOTHER INFORMATION: Clone ID: PAT META530 868976 1
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US-10-437-963-88003/c
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Best Local Sin
Matches 399;
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                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                        GCAGAAGCTGATCCGCGAAGGCGCCCCGCGTGTGTGACGTCGGCGGCGCGCCGGCCTGCCGCGC
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CAAGGACGTGGCCGACGGCGGCGGGAAGTGGTGGGGCGCCGCCGTCGGCGACGCGGC
                                                                    CCTCGGCGACGACAAGAAGAAGCTCCCCCACGGTCCGACCATCCACGTCCGGCTGCAGTT
                                                                                             CGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAGTCGCTCGAAGA
                                                                                                                                                                                                                    CGAGAÁCGTCGTCTTCTCCGTCAAGGTCGCGCTGTCCGTCGATGCCAAGCTCATCGGCCG
                                                                                                                                                                                                                                                      CCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAGCGCATCGGCAT
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                                                                                                                                             CGCCTACCTCCCCGTCAGGGACCTCCTGTCCGGCGAGGCCGTCGAGCGCAAGCTCGACAT
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Pred. No. 3.8e-10;
0; Mismatches 491;
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                                                                                                                                                          ; TYPE: DNA; Cea mays; FEATURE; COTHER INFORMATION: CUS-10-425-115-109294
                                                                                                                                                                                                                                                APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

IITLE OF INVENTION: Nucleic Acid Molecules a

IITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 109294

LENGTH: 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-425-115-109294/c
US-10-425-115-109294, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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                                                                                      Query Match
Best Local S
Matches 308
                                                                                      y Match 6.1%;
Local Similarity 44.1%;
hes 30%; Conservative
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Pred. No. 1.2e-09;
0; Mismatches 391;
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                                                                                                                                                                                                                                                                                                              Sequence 38426, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
 Query Match
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APPLICANT:
APPLICANT:
                                                                                                     TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILLING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 38226
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                                       OTHER INFORMATION: Clone
                                                     ORGANISM: Oryza sativa FEATURE:
                                                                                 TYPE: DNA
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Best Local Similarity Matches 266; Conserv
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0; Mismatches 327;
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Sequence 1, Application US/10156761
Sequence 1, Application US/10156761
Publication NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NO3: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANIAN: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unkno
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RESULT 13
US-10-203-295-1
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Sequence 1, Application US/10203295
Publication No. US20040115762A1
GENERAL INFORMATION:
APPLICANT: Zotchev, Sergey Borisov.
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Pred. No. 5.8e-08;
0; Mismatches 459;
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CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/GB 01/00509
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: GB 0009387.2
PRIOR APPLICATION NUMBER: GB 0009387.2
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
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Best Local Similarity 42.8%;
Matches 404; Conservative
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                           CECTEGAGCECACECTETTCTECEACCATETCEATEACECCAECCTCEACATCTEGEAGA
                                                                                                                                                                                                                                                                     GGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGG----TCACCCAACCGCATCG
                                                                                                                                                                                                                                                                                                                                      TGCGGGTCAGCCACGCCTTCCACTCGCCGCTCATGGACCCGATGCTGGCGGAATTCCGCG
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Fjaervik, Epsen
Brautaset, Trygve
Strom, Arne Reidar
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Sletta, Havard
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Pred. No. 4e-08;
0; Mismatches 537;
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APPLICANT: Strom, Arne Reidar
APPLICANT: Strom, Arne Reidar
APPLICANT: Strom, Arne Reidar
APPLICANT: Strom, Arne Reidar
APPLICANT: Valla, Svein
APPLICANT: Sliingsen, Trond Erling
APPLICANT: Sliingsen, Trond Erling
APPLICANT: Slietta, Havard
APPLICANT: Gulliksen, Ole-Martin
TITLE OF INVENTION: wanipulation and utility
FILE REFERENCE: 1181-265
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT APPLICATION NUMBER: US/10/203,295
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: BB 0010509
PRIOR APPLICATION NUMBER: BB 0002840.7
PRIOR APPLICATION NUMBER: BB 0008786.6
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 49
CORDINATE: DEFENDATE: 2000-04-14
NUMBER OF SEQ ID NOS: 49
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US-10-203-295-35
; Sequence 35, Application US/10203295
; Publication No. US20040115762A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         SEQ ID NO 35
LENGTH: 125401
TYPE: DNA
ORGANISM: Streptomyces noursei ATCC 11455
S-10-203-295-35
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zotchev, Sergey Borisovich
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Fjaervik, Epsen
APPLICANT: Brautaset, Trygve
APPLICANT: Strom, Arne Reidar
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                                                                                                                                                                                                                             Similarity
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  TCGGCATCGAGTTCGACCACGTCAATCTCGACTTCCGCCGCCAGCTCGAGGAAGCCCTAC
                                          CCGGCATCGACGGCCGAGCCCTGGCGCCGCAGCTTCGGCGACAACATCACCTACACCG
                                                                                 ACTGGCGCCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAGCGCA
                                                                                                                           TGGTGATGCTGCCGGAGGGCATGCCCGGTGCCGGCGGCTATCGCGAGCACGACATCCTGA 1141
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Pred. No. 4.5e-08;
0; Mismatches 537;
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US-10-437-963-57011/c

; Sequence 57011, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:
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    APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221) B
FILE REFERENCE: 38-21(53221) B
                                                                                                                                                                                 APPLICANT: La Rosa, Thomas
APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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Zhou, Yihua
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 57011
LENGTH: 1169
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_58865C.1
US-10-437-963-57011
Search completed: November 19,
Job time : 692 secs
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                                                                                                                   1072 ATGGAGC 1078
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                                                                            378 ÁAGGTGC 372
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81.0		σ	AX721949	
80.7	7 1215	σ	AX721941	
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80.		σ	AX721951	AX721951 Sequence
52.8	3 1209	σ	E10020	E10020 DNA encodin
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	AX928131 Sequence		rt	AL939126 Streptomy	AL939128 Streptomy	AF429315 Homo sapi		AF271357 Oryza sat	AK119861 Oryza sat	AE016921 Chromobac	AL939111 Streptomy	AL939105 Streptomy	AE017230 Mycobacte	E17219 gDNA encodi	AB007122 Arthrobac	D14463 Bacillus sp	E01828 Genomic DNA	E01576 DNA sequenc	AF072304 Pseudomon	AF170566 Pseudomon	AE016787 Pseudomon	A01506 Recombinant	I01844 Sequence 2	E00904 gDNA encodi	A10619 Recombinant

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Matches 1211;
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SOGADE, A., YAMAMOTO, K. and Kawamura, Y.
GENE ENCODING CREATINE AMIDINOHYDROLASE
PAtent: JP 1996308579-A 1 26-NOV-1996;
TOYOBO CO LTD
OS Alcaligenes faecalis
PN JP 1996308579-A/1
PD 26-NOV-1996
PF 16-MAY-1995 JP 1995117283
PI SOGABE ATSUSHI, YAMAMOTO KAZUMI, KAWAMOTO, CAZUMI, PROBLEM PROB
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JP 1996308579-A/1

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F 16-MAY-1995 JP 1995117283

F 16-MAY-1995 JP 1995117283

F SCGABE ATSUSHI, YAMAMOTO KAZUMI, KAWAMURA YOSHIHISA PC 12N15/09,C12N1/21,C12N9/78,(C12N15/09,C12R1:05),(C12N1/21,C12N15/09,C12R1:425),
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mat_peptide 1
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amidinohydrolase'.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:511"
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Ricaligenes faecalis gene for creatine amidinohydy
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E13584-1 GI:3252389

JP 1997215494-A/1.

Alcaligenes faecalis
Alcaligenes faecalis
Bacteria; Proteobacteria; Betaproteobacteria; Burl
Alcaligenes en co 1212)
Sogabe,A., Hattori,T., Nishiya,Y. and Kawamura,Y.
NEW CREATINE AMIDINOHYDROLASE, ITS PRODUCTION AND
Patent: JP 1997215494-A/1
PD 19-AUG-1997
PF 13-FEB-1996 JP 1996025435
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                                                                                                                                           GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACACACC
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                                    ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATC
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/mol_type="genomic DNA'
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Pred. No. 2.6e-145;
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Sogabe, A., Nishiya, Y. and Kawamura, Y.

STABLE CREATINE ANIDINCHYDROLASE

Patent: JP 1998174585-A 1 30-JUN-1998;

TOYOBO CO LTD

OS Alcaligenee faecalis
PN JP-1998174585-A/1
PD 30-JUN-1996 JP 1996337027
PF 17-DEC-1996 JP 1996337027
PF 17-DEC-1996 JP 1996337027
PF SOGABE ATSUSHI, NISHIYA YOSHIAKI, KAWAMURA YOSHIHISA PC C12N1/978, CO7H21/04, C12N1/21, C12N15/09//C12Q1/34, (C12N9/78, PC C12N1/19);

PC (C12N1/21, C12R1:19);
PC (STRANGEDEES: Double;
FT Source /organism='Alcaligenee faecalis' FT FT Source /organism='Alcaligenee faecalis' FT
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JP 1998174585-A/1.
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/product='creatine
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/db_xref="taxon:511"
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AUTHORS
Sogabe, A., Yamamoto, K. and Kawamura, Y.
TITLE
Gene encoding creatine amidinohydrolase
JOURNAL
TOYOBO CO LTD
PN JP 2001252088-A 1 18-SEP-2001;
PN JP 2001252088-A/1
PN JP 2001252088-A/1
PD 18-SEP-2001 JP 2001051054
PI ATSUSHI SOGABE, KAZUMI YAMAMOTO, YOSHIHISA KAWAMURA PC C12N15/09, C12N1/21, C12N19/78// (C12N15/09, C12N1/21, PC C12N15/09, C12N1/21, C12N15/00, C12
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/mol_type="genomic DNA"
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18 Sogabe, A., Nishiya, Y. and Kawamura, Y.

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Patent: JP 2001346594-A 1 18-DEC-2001;

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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Koyama, Y. and Furukawa, K.

Direct Submission
Submitted (05-AUG-1998) Yasuji Koyama, Kikkoman Corporation,
Research and Development; Noda 399, Noda, Chiba 278-0037, Ja
(B-mail:dai3-kkm@ga2.so-net.ne.jp, Tel:+81-471-23-5571,
Fax:+81-471-23-5559)
                                                                                                                                                                                                                                                                                                      Alcaligenes sp.
Alcaligenes sp.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                            AB016788
Alcaligenes sp.
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thermostable creatinase
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/organism="Alcaligenes
/mol_type="genomic DNA"
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ALFTSYHCINY'SGWLYCYFGRKYGMVIDHNNATTISAGIDGGGWRRS'SGDNITYIK
WRRDNEYRAURQLITGAKRIGIEEDHVNILDFRRQLEBALFGUEEVDISOSMWRFTIK
SLEEQKLIREGARVCDVGGAACAAAIKAGVPEHEVAIATTNAMIREIAKSFPFVELMD
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DIWEKNVAVHRRGLELIKPGARCKDIAIELNEMYREWDLLKYRSFGYGHSFGVLCHYY
GREAGVELREDIDTELKPGMVVSMEPMVMLPEGMPGAGGYREHDILIVGEDGAENITG
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97.8**%**; 98.6**%**;

Score 1184.8; DB 6; Pred. No. 4.8e-142;

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PI FURNIKAWA KEISUKE, ICHIKAWA TOSHIO, SUZUKI MASARU, KOYAWA TAIJI PC C12N15/09,C12N9/78,C12N19/78,C12R1:19); CC strandedness: Double; CC topology: Linear; CC topology: Linear; FH Key Location/Qualifiers
FT source
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FUTUKAWA, K., ICHIKAWA, T., SUZUKI, M. and KOYAMA, T.,

NOVEL CREATINE AMIDINOHYDROLASE GENE, NOVEL RECOMI
PRODUCTION OF CREATINE AMIDINOHYDROLASE

PALENT: JP 1996089255-A 1 09-APR-1996;

KIKKOMAN CORP

OS Alcaligenes sp. KS-85

PN JP 199608925-A/1

PD 09-APR-1996

PF 29-SEP-1994 JP 1994235737

PI FURUKAWA KEISUKE, ICHIKAWA TOSHIO, SUZUKI MASP
PI CLINI5/09,C12N9/78,(C12N9/78,C12R1:05),(C12N)
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Location/Qualifiers
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Erwinia sp.
Bacteria; Proteobacteria; Ga
Enterobacteriaceae; Erwinia.
TCGGCCGGCATCGACGGCGCCAGCCCTGGCGCCGCAGCTTCGGCGACAACATCACCTAC
                                                                                                             GACGTCGACGCTGCTCACCTCCTATCATTGCATCAATTACTACTCTGGATTCCTG
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DIWEKNVAVHRRGLELIKPGARCKDIAIELNEMYREMDILKYRSFGYGHSFGVLSHYY
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FPFGPEHNIIRN"
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Patent: EP 1298213-A 17 02-APR-2003;
Roche Diagnostice GmbH (DE) ; F.HOFFMANN-LA
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SLEEQKLIREGARICDVGGAACVAAVKAGVPEHEVAIATTNAMVREIAKSFPFVELMD
IWTWFQSGINTDGAHNPVTNRIVQSGDILSLINTFPMIFGYYTALERTLFCCHVDDASL
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/db_xref="taxon:32630"
/note="variant CTqc2"
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Variants of an erwinia-type creatinase
Patent: EP 129813.A 9 02-APR-2003;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA
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Similarity GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACC AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAGCTGATGGACACCTGG GCCTGCGCGGCTGCCATCAAGGCCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCACC CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAG TACTGCTATTTCGGACGCAAGTACGGCATGGTCATCGACCACAACAACGCCACGACGATT ATGACTGACGACATGTTGEACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATC AATGCGATGGTCCGCGAGATCGCCAAGTCGTTCCCCTTCGTCGAACTGATGGACACCTGG GCCTGCGTTGCCGCCGTCAAGGCCGGCGTTCCGGAGCACGAGGTCGCGATCGCCACAACC TCGCTCGAAGAGCAGAAAGCTGATCCGCGAAGGCGCCCGCGTGTGTGACGTCGGCGGCGCG ACCGACTGGCGCCGACAATTTCTATCGCGCCGTGCGCCCAGCTGACCACGGGCGCCAAG TCGGCCGGCATCGACGGCGGCCAGCCCTGGCGCCGCAGCTTCGGCGAACAACATCACCTAC GACGTCGACGCTGCTGCTCCTATCATTGCATCAACTACTACTCTGGATTCCTG TTTTCGGATGCCGAGATGACCCGCCGCCGAAAACGACGTTCGCGGCTGGATGGCCAAGAAC GCGCTGGAGCGAACGCTGTTCTGTGACCACGTCGACGATGCCAGCCTTGACACCTGGGAG GTGCAATCGGGCGATATCCTGTCGCTCAACACGTTCCCGATGATCTTCGGCTACTACACG TCGCTCGAAGAGCAGAAGCTGATCCGCGAGGGTGCCCGTATCTGCGACGTCGGCGGTGCC CTGCCCGGCGTCGAGTTCGTCGATATCGGTCAACCGTCGATGTGGATGCGCACGGTCAAG TCGGCCGGCATCGATGGCGGTCAGCCCTGGCGCCGTAGCTTCGGCGACAACATCACCTAT TACTGCTATTTCGGCCGCAAATACGGCATGGTCATCGACCAGGACCATGCCACGACCATC TTTTCCGATGCCGAGATGACGCCGCCGCCAGAGTGACGTGCGGCGGCTGGATGGCCGAAAAAC Conservative GGCGCCGCGACAACTTCTACCAGGCCGTCCGCCAACTCACCCCCGGCGCCAGG 80.7%; 0; Score 978.4; DB Pred. No. 1e-115; 0; Mismatches 14 146; 6 Length Indels 1215; 0 900 840 840 780 780 720 720 660 660 600 600 540 540 480 480 420 420 360 360 300 300 240 240 180 180 120 120 60 60 0

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   TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC
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Diagnostics GmbH (DE) ; F.HOFFMANN-LA RO
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Patent: EP 1298213-A 21 02-APR-2003;
Roche Diagnostics GmbH (DB) ; F.HOFFMANN-LA
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